



SEQUENCE LISTING

#3

<110> Junghans, Richard P.

<120> Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen

<130> 002

<140> 10/006,771

<141> 2001-12-10

<150> 60/250,090

<151> 2000-11-30

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 7654

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2428)..(3759)

<223> Chimeric IgTCR sequence contained in retroviral vector. Retroviral vector sequence (non-coding regions) are incidental to the invention. The translated (coding region) is relevant to the invention. (pertinent to Figure 3.)

<400> 1

aagcttgcat gcctgcaggt cgactctagg cacataaaga aaaacataac taaccaagct	60
gcagccgaga cagtgaaaag aaccgttaaa acggtttgtt ttaaataaac tgaattattt	120
agagtcattt ctttggtagg aaagtacatt ggcacgtaaa ggagcccaaa gcaatctgtg	180
gaaagcccag gctgggagcc cagcagtttg catcccctcc tggcgtgtac ctaagggttt	240
cttaattgtg tggtttctaa atcttccaga gggtttgtct cattcacttc cacttcggtg	300
cacaatactt ggacgcggat ttactgtctt agcatctatc ggtggccctt cgattgaggc	360
tgaacctgag gcccaattct tcagcttggt aaggagagca caagcaccag aagaggctga	420
cccggcagac ctgtgggcat ttttaacaag ggcctcctgg gtctgtggga ggcaggctta	480

cataaggtgc aaattagaaa tataaataat aagcccatat caatttgtca tcttttttta	540
agctcaagtt ttgaaagacc ccacctgtag gtttggcaag ctagcttaag taacgccatt	600
ttgcaaggca tggaaaatac ataactgaga atagagaagt tcagatcaag gttaggaaca	660
gagagacagc agaatatggg ccaaacagga tatctgtggt aagcagttcc tgccccgctc	720
aggccaaga acagttggaa caggagaata tgggccaac aggatatctg tggtaagcag	780
ttcctgcccc ggctcagggc caagaacaga tgggtccccag atgcggtccc gccctcagca	840
gtttctagag aaccatcaga tgtttccagg gtgccccaaag gacctgaaat gaccctgtgc	900
cttatttgaa ctaaccaatc agttcgcttc tcgcttctgt tcgcgcgctt ctgctccccg	960
agctcaataa aagagcccac aaccctcac tcggcgcgcc agtcctccga tagactgcgt	1020
cgcccgggta cccgtattcc caataaagcc tcttgctgtt tgcattccga tcgtggactc	1080
gctgatacctt gggaggggtct cctcagattg attgactgcc cacctcgggg gtctttcatt	1140
tggaggttcc accgagattt ggagaccctt gcccagggac caccgacccc cccgccggga	1200
ggtaagctgg ccagcaactt atctgtgtct gtccgattgt ctagtgtcta tgactgattt	1260
tatgcgcctg cgtcgggtact agttagctaa ctagctctgt atctggcgga cccgtgggtg	1320
aactgacgag ttcggaacac ccggccgcaa ccctgggaga cgtcccaggg acttcggggg	1380
ccgtttttgt ggcccagact gagtcctaaa atcccgatcg tttaggactc tttggtgcac	1440
cccccttaga ggagggatat gtggttctgg taggagacga gaacctaaaa cagttcccgc	1500
ctccgtctga atttttgctt tcggtttggg accgaagccg cgccgcgcgt cttgtctgct	1560
gcagcatcgt tctgtgttgt ctctgtctga ctgtgtttct gtatttgtct gaaaatatgg	1620
gcccgggcta gactgttacc actcccttaa gtttgacctt aggtcactgg aaagatgtcg	1680
agcggatcgc tcacaaccag tcggtagatg tcaagaagag acgttgggtt accttctgct	1740
ctgcagaatg gccaaccttt aacgtcggat ggccgcgaga cggcaccttt aaccgagacc	1800
tcatacccca ggttaagatc aaggtctttt cacctggccc gcatggacac ccagaccagg	1860
tcccctacat cgtgacctgg gaagccttgg cttttgacct ccctccctgg gtcaagccct	1920

ttgtacaccc taagcctccg cctcctcttc ctccatccgc cccgtctctc ccccttgaac	1980
ctcctcggtc gaccccgccg cgatcctccc tttatccagc cctcactcct tctctaggcg	2040
cccccatatg gccatattgag atcttatatg gggcaccccc gcccttgta aacttccttg	2100
accctgacat gacaagagtt actaacagcc cctctctcca agctcactta caggcttcta	2160
cttagtccag cacgaagtct ggagacctct ggcggcagcc taccaagaac aactggaccg	2220
accggtggta cctcaccctt accgagtcgg cgacacagtg tgggtccgcc gacaccagac	2280
taagaacctt gaacctcgct ggaaaggacc ttacacagtc ctgctgacca ccccaccgc	2340
cctcaaagta gacggcatcg cagcttgat acacgccgcc cacgtgaagg ctgccgaccc	2400
cgggggtgga ccctcctcta gactgcc atg gga tgg agc tgt atc atc ctc ttc	2454
Met Gly Trp Ser Cys Ile Ile Leu Phe	
1 5	
ttg gta gca aca gct aca ggt gtc cac tcc gac atc cag ctg acc cag	2502
Leu Val Ala Thr Ala Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln	
10 15 20 25	
agc cca agc agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc	2550
Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr	
30 35 40	
tgt aag gcc agt cag gat gtg ggt act tct gta gct tgg tac cag cag	2598
Cys Lys Ala Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln	
45 50 55	
aag cca ggt aag gct cca aag ctg ctg atc tac tgg aca tcc acc cgg	2646
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg	
60 65 70	
cac act ggt gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac	2694
His Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp	
75 80 85	
ttc acc ttc acc atc agc agc ctc cag cca gag gac atc gcc acc tac	2742
Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr	
90 95 100 105	
tac tgc cag caa tat agc ctc tat cgg tcg ttc ggc caa ggg acc aag	2790
Tyr Cys Gln Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys	
110 115 120	

gtg gaa atc aaa cga ggt ggc tca gga tcg ggt gga tcc ggc tct ggt	2838
Val Glu Ile Lys Arg Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Gly	
125 130 135	
ggc tca gga tcg gag gtc caa ctg gtg gag agc ggt gga ggt gtt gtg	2886
Gly Ser Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val	
140 145 150	
caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc gat	2934
Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp	
155 160 165	
ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct gga aaa ggt	2982
Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly	
170 175 180 185	
ctt gag tgg att gga gaa att cat cca gat agc agt acg att aac tat	3030
Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr	
190 195 200	
gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac aac gcc aag	3078
Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys	
205 210 215	
aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa gac acc ggg	3126
Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly	
220 225 230	
gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg ttt gct tat	3174
Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr	
235 240 245	
tgg ggc caa ggg acc ccg gtc acc gtc tcc agt gct aag ccc acc acg	3222
Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Lys Pro Thr Thr	
250 255 260 265	
acg cca gcg ccg cga cca cca aca ccg gcg ccc acc atc gcg tcg cag	3270
Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln	
270 275 280	
ccc ctg tcc ctg cgc cca gag gcg gct cgg cca gcg gcg ggg ggc gca	3318
Pro Leu Ser Leu Arg Pro Glu Ala Ala Arg Pro Ala Ala Gly Gly Ala	
285 290 295	
gtg cac acg agg ggg ctg gac ttc gcc ctg gat ccc aaa ctc tgc tac	3366
Val His Thr Arg Gly Leu Asp Phe Ala Leu Asp Pro Lys Leu Cys Tyr	
300 305 310	

ctg ctg gat gga atc ctc ttc atc tat ggt gtc att ctc act gcc ttg	3414
Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu	
315 320 325	
ttc ctg aga gtg aag ttc agc agg agc gca gag ccc ccc gcg tac cag	3462
Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln	
330 335 340 345	
cag ggc cag aac cag ctc tat aac gag ctc aat cta gga cga aga gag	3510
Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu	
350 355 360	
gag tac gat gtt ttg gac aag aga cgt ggc cgg gac cct gag atg ggg	3558
Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly	
365 370 375	
gga aag ccg aga agg aag aac cct cag gaa ggc ctg tac aat gaa ctg	3606
Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu	
380 385 390	
cag aaa gat aag atg gcg gag gcc tac agt gag att ggg atg aaa ggc	3654
Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly	
395 400 405	
gag cgc cgg agg ggc aag ggg cac gat ggc ctt tac cag ggt ctc agt	3702
Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser	
410 415 420 425	
aca gcc acc aag gac acc tac gac gcc ctt cac atg cag gcc ctg ccc	3750
Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro	
430 435 440	
cct cgc taa ctgcacgcgg ccgcggatcc ggattagtcc aatttggttaa	3799
Pro Arg	
agacaggata tcagtgggtcc aggctctagt ttgactcaa caatatcacc agctgaagcc	3859
tatagagtac gagccataga taaaataaaa gattttatatt agtctccaga aaaagggggg	3919
aatgaaagac cccacctgta ggtttggtgcaa gctagcttaa gtaacgccat ttgcaaggc	3979
atggaaaata cataactgag aatagagaag ttcagatcaa ggtaggaac agagagacag	4039
cagaatatgg gccaaacagg atatctgtgg taagcagttc ctgccccgct cagggccaag	4099
aacagttgga acaggagaat atggggccaaa caggatatct gtggtaagca gttcctgccc	4159

cggctcaggg	ccaagaacag	atgggtcccca	gatgcggtcc	cgccctcagc	agtttctaga	4219
gaaccatcag	atgtttccag	ggtgccccaa	ggacctgaaa	tgaccctgtg	ccttatttga	4279
actaaccaat	cagttcgctt	ctcgcttctg	ttcgcgcgct	tctgctcccc	gagctcaata	4339
aaagagccca	caaccctca	ctcggcgcgc	cagtcctccg	atagactgcg	tcgcccgggt	4399
acccgtgttc	tcaataaacc	ctcttgacgt	tgcacccgac	tcgtgggtctc	gctgttcctt	4459
gggaggggtct	ctctgagtg	ttgactaccc	gtcagcgggg	tctttcagtt	tctcccacct	4519
acacaggtct	cactaacatt	cctgatgtgc	cgcagggact	ccgtcagccc	ggtttttgtt	4579
tataataaaa	tgcaagaaca	gtgttcctt	caagccagac	tacatcctga	ctctcggctt	4639
tataaaagaa	tggtgaagg	ctctgtggac	tatctgccac	acgacttttt	aagattttta	4699
tgctcctgg	atgagggatt	tagtcaatct	atcctcgtct	attttgctgg	cttctccgta	4759
ttttaaat	ctagtttgca	ctcccttct	gagagcacgg	cgattgcaga	gtagttaata	4819
ctctgagggc	aggcttctgt	gaaaagggtg	cctgggctca	gtgtgagatt	ttgccataaa	4879
aaggggtcct	gcccctgtgt	acagacagat	cggaatctag	agtgcatact	cagagtcccc	4939
gcggttcgg	ggctctgatc	tcagggcatc	tttgcttaga	gatcctctac	gccggacgca	4999
tcgtggccgg	gtaccgagct	cgaattcgta	atcatgggtca	tagctgtttc	ctgtgtgaaa	5059
ttgttatccg	ctcacaattc	cacacaacat	acgagccgga	agcataaagt	gtaaagcctg	5119
gggtgcctaa	tgagtgagct	aactcacatt	aattgcgttg	cgctcactgc	ccgctttcca	5179
gtcgggaaac	ctgtcgtgcc	agctgcatta	atgaatcggc	caacgcgcgg	ggagaggcgg	5239
tttgcgtatt	gggcgtctt	ccgcttcctc	gctcactgac	tcgctgcgct	cggtcgttcg	5299
gctgcggcga	gcggtatcag	ctcactcaaa	ggcggtaata	cggttatcca	cagaatcagg	5359
ggataacgca	ggaaagaaca	tgtgagcaaa	aggccagcaa	aaggccagga	accgtaaaaa	5419
ggccgcgttg	ctggcgtttt	tccataggct	ccgccccct	gacgagcatc	acaaaaatcg	5479
acgctcaagt	cagaggtggc	gaaacccgac	aggactataa	agataccagg	cgtttccccc	5539
tggaagctcc	ctcgtgcgct	ctcctgttcc	gaccctgccg	cttaccggat	acctgtccgc	5599

ctttctccct tcggaagcg tggcgctttc tcatagctca cgctgtaggt atctcagttc	5659
ggtgtaggtc gttcgctcca agctgggctg tgtgcacgaa cccccggtc agcccgaccg	5719
ctgcgcctta tccggttaact atcgtcttga gtccaacccg gtaagacacg acttatcgcc	5779
actggcagca gccactggta acaggattag cagagcgagg tatgtaggcg gtgctacaga	5839
gttcttgaag tgggtggccta actacggcta cactagaagg acagtatttg gtatctgcgc	5899
tctgctgaag ccagttacct tcggaaaaag agttggtagc tcttgatccg gcaaacaaac	5959
caccgctggt agcgggtggt tttttgtttg caagcagcag attacgcgca gaaaaaagg	6019
atctcaagaa gatcctttga tcttttctac ggggtctgac gctcagtgga acgaaaactc	6079
acgttaaggg attttgggtca tgagattatc aaaaaggatc ttcacctaga tccttttaaa	6139
ttaaaaatga agttttaaat caatctaaag tatatatgag taaacttgggt ctgacagtta	6199
ccaatgctta atcagtgagg cacctatctc agcgatctgt ctatttcgtt catccatagt	6259
tgctgactc cccgtcgtgt agataactac gatacgggag ggcttaccat ctggccccag	6319
tgctgcaatg ataccgcgag acccacgctc accggctcca gatttatcag caataaacca	6379
gccagccgga agggccgagc gcagaagtgg tcctgcaact ttatccgcct ccatccagtc	6439
tattaattgt tgccgggaag ctagagtaag tagttcgcca gttaatagtt tgcgcaacgt	6499
tgttgccatt gctacaggct cgtggtgtca cgctcgtcgt ttggtatggc ttcattcagc	6559
tccggttccc aacgatcaag gcgagttaca tgatcccca tgttggtgcaa aaaagcggtt	6619
agtccttcg gtcctccgat cgttgtcaga agtaagttgg ccgcagtgtt atcactcatg	6679
gttatggcag cactgcataa ttctcttact gtcatgccat ccgtaagatg cttttctgtg	6739
actggtgagt actcaaccaa gtcattctga gaatagtgtg tgcggcgacc gagttgctct	6799
tgcccggcgt caatacggga taataccgcg ccacatagca gaactttaaa agtgctcatc	6859
attggaaaac gttcttcggg gcgaaaactc tcaaggatct taccgctgtt gagatccagt	6919
tcgatgtaac ccactcgtgc acccaactga tcttcagcat cttttacttt caccagcggt	6979
tctgggtgag caaaaacagg aaggcaaaat gccgcaaaaa agggaataag ggcgacacgg	7039

```

aatgttgaa tactcatact cttccttttt caatattatt gaagcattta tcagggttat 7099
tgtctcatga gcggatacat atttgaatgt atttagaaaa ataaacaaat aggggttccg 7159
cgcacatttc cccgaaaagt gccacctgac gtctaagaaa ccattattat catgacatta 7219
acctataaaa ataggcgtat cacgaggccc ttctgtctcg cgcgttttcgg tgatgacggt 7279
gaaaacctct gacacatgca gctcccggag acggtcacag cttgtctgta agcggatgcc 7339
gggagcagac aagcccgtca gggcgcgtca gcgggtgttg gcgggtgtcg gggctggctt 7399
aactatgcgg catcagagca gattgtactg agagtgcacc atatgcggtg tgaaataccg 7459
cacagatgcg taaggagaaa ataccgcatc aggcgccatt cgccattcag gctgcgcaac 7519
tgttgggaag ggcgatcggg gcgggcctct tcgctattac gccagctggc gaaaggggga 7579
tgtgctgcaa ggcgattaag ttgggtaacg ccagggtttt cccagtcacg acgttgtaaa 7639
acgacggcca gtgcc 7654

```

```

<210> 2
<211> 443
<212> PRT
<213> Homo sapiens

```

<400> 2

```

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1           5           10          15

```

```

Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
          20          25          30

```

```

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
          35          40          45

```

```

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
          50          55          60

```

```

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg

```


65		70		75		80
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser						
		85		90		95
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu						
		100		105		110
Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly						
		115		120		125
Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Glu Val Gln						
		130		135		140
Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg						
		145		150		155
Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser						
		165		170		175
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile						
		180		185		190
His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg						
		195		200		205
Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln Met						
		210		215		220
Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu						
		225		230		235
Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val						
		245		250		255
Thr Val Ser Ser Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro Pro						

260	265	270
Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu		
275	280	285
Ala Ala Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp		
290	295	300
Phe Ala Leu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe		
305	310	315
Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe Ser		
325	330	335
Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr		
340	345	350
Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys		
355	360	365
Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn		
370	375	380
Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu		
385	390	395
Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly		
405	410	415
His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr		
420	425	430
Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg		
435	440	

<210> 3

<211> 422
 <212> DNA
 <213> Homo sapiens and Mus sp.

 <220>
 <221> CDS
 <222> (8)..(421)
 <223> hMn14 VH, humanized (CDR-grafted) anti-CEA antibody heavy chain V region (aa20-138) with leader (aa1-19) (pertinent to Fig. 4A.)

<400> 3
 cctcacc atg gga tgg agc tgt atc atc ctc ttc ttg gta gca aca gct 49
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala
 1 5 10

 aca ggt gtc cac tcc gag gtc caa ctg gtg gag agc ggt gga ggt gtt 97
 Thr Gly Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val
 15 20 25 30

 gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc 145
 Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe
 35 40 45

 gat ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct gga aaa 193
 Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys
 50 55 60

 ggt ctt gag tgg att gga gaa att cat cca gat agc agt acg att aac 241
 Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn
 65 70 75

 tat gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac aac gcc 289
 Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala
 80 85 90

 aag aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa gac acc 337
 Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr
 95 100 105 110

 ggg gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg ttt gct 385
 Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala
 115 120 125

 tat tgg ggc caa ggg acc ccg gtc acc gtc tcc tca g 422
 Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser
 130 135

<210> 4
 <211> 138
 <212> PRT
 <213> Homo sapiens and Mus sp.

<400> 4

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
 20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe
 35 40 45

Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr Ala
 65 70 75 80

Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
 85 90 95

Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val
 100 105 110

Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp
 115 120 125

Gly Gln Gly Thr Pro Val Thr Val Ser Ser
 130 135

<210> 5
 <211> 712
 <212> DNA
 <213> Homo sapiens and Mus sp.

<220>
 <221> CDS
 <222> (14)..(712)
 <223> hMN14 VLCK, humanized (CDR-grafted) anti-CEA antibody kappa light chain V region (aa20-126), with human constant CK domain (aa127-232) and leader (aa1-19). (pertinent to Figure 4B.)

<400> 5
 tctagacctc acc atg gga tgg agc tgt atc atc ctc ttc ttg gta gca 49
 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala
 1 5 10

aca gct aca ggt gtc cac tcc gac atc cag ctg acc cag agc cca agc 97
 Thr Ala Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser
 15 20 25

agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt aag gcc 145
 Ser Leu Ser Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala
 30 35 40

agt cag gat gtg ggt act tct gta gct tgg tac cag cag aag cca ggt 193
 Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly
 45 50 55 60

aag gct cca aag ctg ctg atc tac tgg aca tcc acc cgg cac act ggt 241
 Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly
 65 70 75

gtg cca agc aga ttc agc ggt agc ggt agc ggt acc gac ttc acc ttc 289
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe
 80 85 90

acc atc agc agc ctc cag cca gag gac atc gcc acc tac tac tgc cag 337
 Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
 95 100 105

caa tat agc ctc tat cgg tcg ttc ggc caa ggg acc aag gtg gaa atc 385
 Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile
 110 115 120

aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat 433
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 125 130 135 140

gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac 481
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn

	145	150	155	
ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc				529
Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu				
	160	165	170	
caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac				577
Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp				
	175	180	185	
agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac				625
Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr				
	190	195	200	
gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc				673
Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser				
	205	210	215	220
tcg ccc gtc aca aag agc ttc aac agg gga gag tgt taa				712
Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys				
	225	230		

<210> 6
 <211> 232
 <212> PRT
 <213> Homo sapiens and Mus sp.

<400> 6

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
1 5 10 15

Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
20 25 30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
35 40 45

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
50 55 60

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
85 90 95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu
100 105 110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val
115 120 125

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
130 135 140

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
145 150 155 160

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
165 170 175

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
180 185 190

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
195 200 205

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
210 215 220

Lys Ser Phe Asn Arg Gly Glu Cys
225 230